

# Localization of the human TAX-1 gene to 1q32.1: a region implicated in microcephaly and Van der Woude syndrome

Susan Kenwrick\*, Margaret Leversha<sup>1</sup>, Lesley Rooke<sup>2</sup>, Thomas Hasler<sup>3</sup> and Peter Sonderegger<sup>3</sup>

Department of Medicine, University of Cambridge, Addenbrooke's Hospital, Cambridge CB2 2QQ, <sup>1</sup>Department of Pathology, University of Cambridge, Cambridge, <sup>2</sup>Imperial Cancer Research Fund, Clire Hall Laboratories, South Mimms, Potters Bar, Hertfordshire EN8 3LD, UK and <sup>3</sup>Biochemisches Institut der Universität Zurich, Winterthurerstrasse 190, CH-8057, Zurich, Switzerland

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Cell adhesion molecules TAX-1 (1), TAG-1 (2) and axonin-1 (3) are homologous cell surface glycoproteins expressed in the neural tissue of human, rat and chicken respectively. They are members of a family of proteins composed of repeated immunoglobulin-like (IgC2) and fibronectin type III-like (FNIII) domains that mediate adhesion between components of the nervous system (4). Studies of neurite outgrowth on immobilized axonin-1 indicate that it participates in a heterophilic interaction with L1, a related member of the immunoglobulin superfamily that is expressed on the axons of migrating neurones (5). Recently, we demonstrated that mutations in the human L1 gene give rise to X-linked hydrocephalus, a congenital disorder of brain development (6, 7). In view of the structural similarity and functional association between L1 and TAX-1 homologues we anticipate that disruption of TAX-1 would also result in developmental impairment. As a first step towards determining whether TAX-1 is associated with a genetically mapped inherited disorder we have established its chromosomal location.

Oligonucleotide primers specific for TAX-1 (EMBL accession no. X68274) were used in polymerase chain reactions (PCRs) to

amplify a 255 bp product from human DNA. Primers that flank the stop codon (cactcgtggcgatgctgacctc, forward and atcctgctgggttctatctcgg, reverse) were chosen in order to avoid introns. PCRs using DNA from a panel of somatic cell hybrids indicated that the TAX-1 locus resides on chromosome 1 (Figure 1). Confirmation and refinement of this localization was obtained by fluorescent *in situ* hybridization of a 4.5 kb TAX-1 cDNA clone to metaphase chromosomes. A single band of fluorescence was seen in all cells in the proximal section of 1q32 (1q32.1, Figure 2).

A literature search revealed that the gene for human myosin-binding protein H (MyBP-H), another member of the IgC2/FNIII repeat family, resides within 1q32.1. More interesting, however, is the association of two morphogenetic abnormalities with this region. Van der Woude syndrome, a defect of craniofacial development thought to result from aberrant neural crest cell migration, is genetically linked to 1q32.1 (8) and studies of deletion and translocation events indicate that a gene for microcephaly with mental retardation also resides in this region (9, 10). In view of its potential role in cell migration analysis of the TAX-1 gene in these cases is warranted.

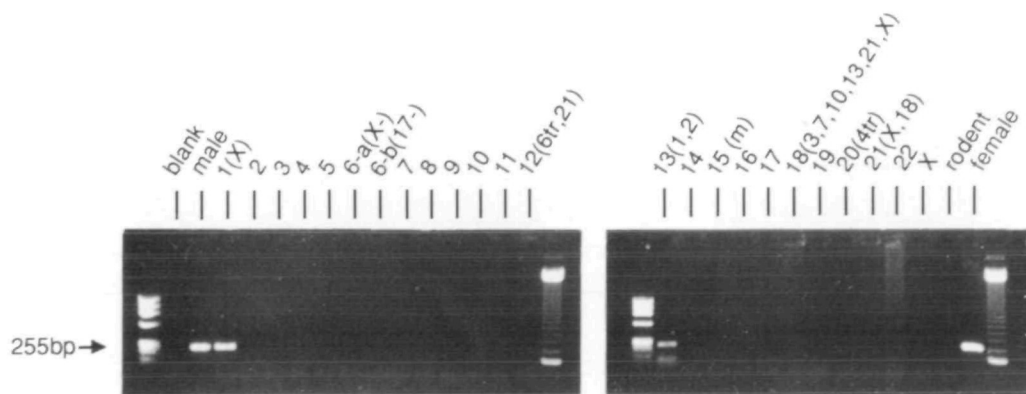


Figure 1. PCR amplification of 255 bp of the TAX-1 locus from genomic DNA. PCRs utilized 10 ng of DNA, and 2 pmols of each primer in 10  $\mu$ l commercial buffer (Promega) with annealing at 65°C. Human lanes are labelled male and female. Rodent is a mixture of mouse and hamster. The components of hybrids are shown above each lane, the primary mapping chromosome followed by additional components in parentheses. '-' indicates an incomplete chromosome, 'tr' trace quantities and 'm' a marker chromosome. 6-a plus 6-b represents an entire 6. Full details of the hybrids can be obtained from L.R. Molecular weight markers are Hae III-digested  $\phi$ X174 and a 123 bp ladder.

\* To whom correspondence should be addressed

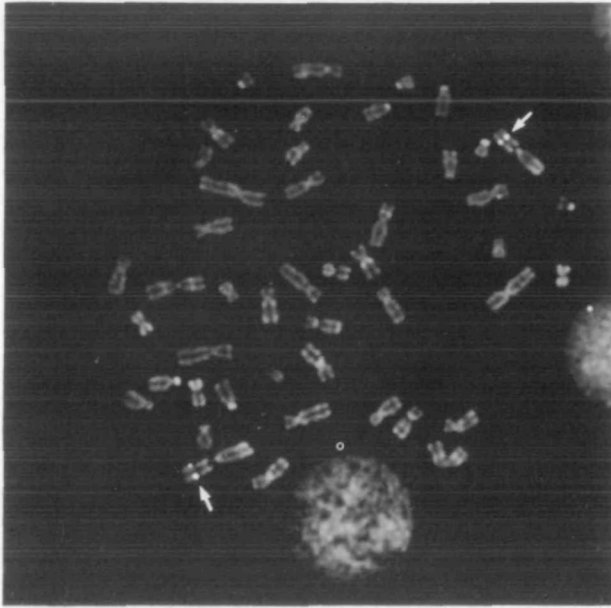


Figure 2. Fluorescent hybridization of TAX-1 cDNA to metaphase chromosomes from a male lymphoblastoid cell line using the method of Fan *et al.* (11).

## REFERENCES

1. Hasler, T.H., Rader, C., Stoeckli, E.T., Zueligg, R.A. and Sonderegger, P. (1993) *Eur. J. Biochem.* 211, 329–339.
2. Furlley, A.J., Morton, S.B., Manalo, D., Karagogeos, D., Dodd, J. and Jessel, T.M. (1990) *Cell* 61, 157–170.
3. Zueligg, R.A., Rader, C., Schroeder, A., Kalousek, M.B., von Bohlen und Halbach, F., Osterwalder, T. *et al.* (1992) *Eur. J. Biochem.* 204, 453–463.
4. Sonderegger, P.R. and Rathjen, F.G. (1992) *J. Cell Biol.* 119, 1387–1394.
5. Kuhn, T.B., Stoeckli, E.T., Condrau, M.A., Rathjen, F.G. and Sonderegger, P. (1991) *J. Cell Biol.* 115, 1113–1126.
6. Rosenthal, A., Jouet, M. and Kenrick, S. (1992) *Nature Genet.* 2, 107–112.
7. Jouet, M., Rosenthal, A., MacFarlane, J., Donnai, D. and Kenrick, S. (1993) *Nature Genet.* in press.
8. Sander, A., Moser, H., Liechti-Gallati, S., Grimm, T., Zingg, M. and Ravet, J. (1993) *Hum. Genet.* 91, 55–62.
9. Fennell, S.J., Malcolm, S., Williamson, R. and Ferguson-Smith, M.A. (1979) *J. Med. Genet.* 16, 246–253.
10. Perez-Castillo, A., Angeles Martin-Lucas, M. and Abrisqueta, J.A. (1984) *Hum. Genet.* 67, 230–232.
11. Fan, Y., Davis, L.M. and Shows, T.B. (1990) *Proc. Natl. Acad. Sci. USA* 87, 6223–6227.